

Substitute_Sequence_Listing.TXT

SEQUENCE LISTING

<110> Yoshinori Watanabe

<120> Novel centromeric protein SHUGOSHIN

<130> 4439-4043

<140> 10/581,158

<141> 2007-01-30

<150> JP2003-401943

<151> 2003-12-01

<150> JP2004-279450

<151> 2004-09-27

<160> 45

<170> PatentIn version 3.1

<210> 1

<211> 960

<212> DNA

<213> yeast

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<210> 2

<211> 319

<212> PRT

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<213> yeast

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Ile Lys Ile Asn Thr Gln Leu Ser Ile Lys Ile Arg Glu Ser Glu Asn
35 40 45

Glu Ile Gln Asp Leu Ile Gln Glu Asn Phe Thr Leu Lys Ser Tyr Leu
50 55 60

Val Lys Leu Glu Ala Arg Phe Arg Asn Gln Ser Gln Thr Glu Asp Leu
65 70 75 80

Leu Lys Asn Phe Phe Pro Glu Ile Gln Thr Ile His Lys Lys Ile Ser
85 90 95

Gln Val Gln Ser Leu Leu Lys Ile Ile Glu Lys Lys Cys Ser Ser Asp
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Phe Leu Glu Ala Asn Val Lys Ser Gln Phe Thr Thr Cys Glu Asn Lys
115 120 125

Asp Ser Lys Glu Asp Tyr Gln Ile Leu His Asn Lys Arg Leu Glu Tyr
130 135 140

Val Ser Phe Asn Asp Glu Leu Lys Ser Leu Glu Thr Gly Gln Pro Leu
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Tyr Cys Phe Gln Asp Phe Gln Lys Lys Val His Gly Pro Pro Ala Leu
165 170 175

Ser Glu Lys Pro Gly Lys Cys Ile Leu Lys Asp Lys Thr Asn Ala His
180 185 190

Val Asn Lys Ile Pro Gln Asp Glu Val Asn Tyr Ser Leu Pro Gln Lys
195 200 205

Asn Ile Thr Ile Phe Ser Lys Glu Leu Lys Glu Asn Glu Phe Glu Ser
210 215 220

Ile Asn Glu Gly Glu Thr Glu Glu Glu Lys Ala Lys Thr Ser Asn Val
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Gly Gln Ala Thr Gly Asp Ser Ser Pro Cys Asp Phe Glu Glu Ser Gln
260 265 270

Pro Arg Ile Asn Gly Arg Glu Lys Leu Arg Arg Ser Val Lys Val Ile
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Asn Tyr Ala Ile Pro Ser Leu Arg Thr Lys Leu Arg Arg Asp Phe Asp
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Substitute_Sequence_Listing.TXT

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 <212> PRT
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Ile Arg Ile Lys Glu Leu Gln Leu Glu Asn Glu Arg Leu Leu Ser Glu
 35 40 45

Asn Ile Asp Leu Arg Thr Thr Ala Ile Asn Leu Glu Glu Gln Leu Glu
 50 55 60

Thr Val Gln Asn Glu Asn Glu Glu Asn Lys Thr Lys Leu Ala Ala Leu
 65 70 75 80

Leu Asn Arg Phe His Glu Glu Thr Asp Asn Phe Leu Ser Lys Leu Ser
 85 90 95

Leu Cys Gln Gln Glu Ile Gln Asp Thr Phe Lys Pro Val Glu Ala Asn

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105

110

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Val Val Lys Asp Thr Glu Glu Ile Ile Glu Gln Ala Gln His Asp Val
 130 135 140

Ser Leu Arg Asn Leu Ser Gly Ile Glu Asp Glu Asn Ile Ile Asp Asp
 145 150 155 160

Gly Glu Thr Ala Ile Asn Glu Gln Lys Lys Arg Glu Ala Asn Val Phe
 165 170 175

Ser Asp Thr Gln Ser Ala Pro Gln Leu Lys Ser Gly Lys Ala Leu Pro
 180 185 190

Ala Asp Phe Glu Asn Pro Tyr Asn Leu Ser Asn Ser Lys Pro Val Asn
 195 200 205

Asn Asn Asn Glu Asp Arg Val Glu Ala Val Thr Ser Glu Asn Lys Ser
 210 215 220

Ile Asp Ser Ala Pro Gln Glu Lys Asn His Glu Tyr Glu Ile Val Ser
 225 230 235 240

Pro Lys Ser Leu Ser Asn Lys Ile Asn Asn Gln Ala Ala Ala Gln Arg
 245 250 255

Arg Thr Glu Glu Asp Asn Ala Asn Gly Val Ala Gln Glu Glu Asn Glu
 260 265 270

Gly Ser Gln Glu Ala His Phe His Ser Arg Ile Gln Ser Asp Thr Val
 275 280 285

Ile Gln Ser Thr Pro Thr Lys Arg Lys Trp Asp Val Asp Ile Gln Asn
 290 295 300

Lys Gln Ile Asn Leu Ala Ser Ala Ala Thr Asn Val Thr Gly Tyr Val
 305 310 315 320

Ser Glu Thr Asp Ser Arg Pro Asn Arg Ala Asn Ser Leu Asp Ser Ala
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Val Leu Leu Val Gln Ser Ser Asn Lys Ser Asn Arg Asn Gly His His
 340 345 350

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Ile Ser Asp Pro Asn Leu Asn Ser Ser Ile Ser Leu Lys Phe Ala Pro
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Glu Asp Thr Ala His Asn Ser Leu Thr Ser Gln Glu Asn Val Gly Pro
370 375 380

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385 390 395 400

Arg Thr Asp Thr Pro Arg Glu Ile Asn Gly Leu Val Asp Ser Ser Val
405 410 415

Thr Asn Gly Asn Glu Lys Phe Ser Val Glu Ile Met Asn Asp Ser Asn
420 425 430

Lys Ile Gly Leu Asn Pro Lys Ser Phe Thr Asp Glu Glu Arg Glu Ile
435 440 445

Leu Thr Leu Phe Arg Asn Pro Pro Met Arg Leu Ser Ser Glu Pro Pro
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Ser Ser Asn Gly Phe Ser Ile Ala His Pro Asn Asn Ser Pro Leu Arg
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Pro Pro Ser Leu Gln Gly Ile Leu Asn Ala Glu Asp Arg Pro Tyr Glu
485 490 495

Ile Glu Pro Ser Arg Ser Ser Phe Ala Thr Asn Asp Thr Gly Ser Tyr
500 505 510

Asn Asn Leu Glu Leu Leu Ser Ser Val Thr Asn Leu Lys Ser Pro Asn
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Glu Asn Asp Arg Val Thr Lys Thr Gln Ser Arg Arg Glu Thr Lys Val
530 535 540

Lys Arg Arg Arg Lys Ala Arg Ile Gln Glu Thr Ser Glu Glu Ser Thr
545 550 555 560

Val Val Asn Glu Pro Asn Glu Lys Pro Asp Gly Arg Ser Arg Arg Glu
565 570 575

Arg Lys Lys Val Asn Tyr Ala Leu Pro Gly Leu Arg Thr Lys Leu Arg
580 585 590

Arg Asn Phe Asp Leu Pro Ser Asp His Val Lys Ala Lys Lys Thr Arg
595 600 605

Substitute_Sequence_Listing.TXT

Arg Ala Pro Lys Asn Ser Glu Asn Asp Ser Ala Thr Lys Thr Glu Thr
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Ala Asn Ile Thr Ser Glu Ala Pro Thr Thr Ser Glu Val Thr Leu Glu
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Asn Ser Glu Thr Leu Asn Leu
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Substitute_Sequence_Listing.TXT

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aagtcaacaa gaactaaaaa attgttcaaa aatgcaattg tcaataatth atctgatgaa	1560
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<400> 6

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			20					25					30		

Met	Asp	Leu	Glu	Ser	Gln	Lys	Val	Glu	Asn	Ile	Arg	Gln	Ser	Tyr	Ser
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Arg	Gln	Asn	Ser	Leu	Leu	Ala	Lys	Asp	Asn	Ser	Ile	Leu	Lys	Ile	Lys
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Val	Asn	Ser	Leu	Glu	Lys	Lys	Ile	Ser	Gln	Leu	Val	Gln	Glu	Asn	Val
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Thr	Leu	Arg	Ser	Lys	Thr	Ser	Ile	Ser	Glu	Ala	Ile	Tyr	Arg	Glu	Arg
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Leu	Ser	Asn	Gln	Leu	Gln	Val	Ile	Glu	Asn	Gly	Ile	Ile	Gln	Arg	Phe
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Asp	Glu	Ile	Phe	Tyr	Met	Phe	Glu	Asn	Val	Arg	Lys	Asn	Glu	Asn	Leu
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Pro	Ser	Ser	Ser	Leu	Arg	Thr	Met	Leu	Lys	Arg	Thr	Ser	Ser	Arg	Ser
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Arg	Ser	Cys	Ser	Leu	Ser	Ser	Pro	Thr	Tyr	Ser	Lys	Ser	Tyr	Thr	Arg
145					150					155					160

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 Asp Asp Gly Pro Asp Leu Glu Pro Lys Ala Lys Lys Arg Lys Ser Ser
 180 185 190
 Arg Arg Gln Ser Met Phe Val Ser Thr Ser Leu Glu Pro Glu Asp Glu
 195 200 205
 Thr Gly Glu Asn Glu Pro Met Met Glu Asn Ser Ser Val Glu Val Pro
 210 215 220
 Ala Glu Ser His Glu Ser Ala Gln Val Glu Glu Thr Ile Asp Ala Leu
 225 230 235 240
 Asn Pro Glu Glu Glu Asn Ser Asp Ser Val Ser Asn Phe Thr Asn Ser
 245 250 255
 Ile Ile Glu Tyr Ser Ile Pro Glu Glu Asn Pro Thr Glu Pro Glu His
 260 265 270
 Ser Ser Ser Lys Leu Glu Ile Phe Asn Asp Ser Thr Asn Met Leu Ser
 275 280 285
 Thr Val Pro Ser Asn Pro Leu Pro Leu Pro Leu Pro Gly Pro Ser Ala
 290 295 300
 Thr Leu Pro Thr Thr Thr Ser Asp Ala Ser Thr Val Tyr Pro Ser Ser
 305 310 315 320
 Ser Ser Ser Thr Asn Ser His Pro Lys Thr Lys Ile Lys His Ser Met
 325 330 335
 Lys Pro Pro Arg Ile Glu Leu Lys Lys Lys Val Ile Asp Glu Val Met
 340 345 350
 Pro Val Ser Asn Met Ser Ser Asn Ser Glu Ile Ser Phe Thr Arg Thr
 355 360 365
 Arg Arg Thr Arg Gly Lys Ala Val Asp Tyr Thr Leu Pro Ser Leu Arg
 370 375 380
 Ala Lys Met Arg Arg Pro Ser Glu Lys Leu Val Asp Ala Thr Thr Val
 385 390 395 400
 Ile Asp Ile His Asp Leu Gln Val Ser Lys Arg Asn Arg Glu Thr Ser
 405 410 415

Substitute_Sequence_Listing.TXT

His Lys Arg Lys Ser Leu Ser Gln Asp Ser Ile Pro Asp Glu Pro Gln
420 425 430

Leu Arg Glu Val Val Val Ser Lys Asp Tyr Gly Thr Pro Lys Gly Lys
435 440 445

Lys Thr Glu Asp Glu Ile His Glu Asp Thr Ala His Leu Met Thr Thr
450 455 460

Ser Asn Asn Asn Ser Asn Asn Lys Asn Glu Lys Lys Leu Thr Ser Asn
465 470 475 480

Asn Ser Pro Lys Lys Ser Ser Pro Leu Leu Asp Ile Thr Asn Lys Ser
485 490 495

Glu Asn Lys Lys Lys Ser Thr Arg Thr Lys Lys Leu Phe Lys Asn Ala
500 505 510

Ile Val Asn Asn Leu Ser Asp Glu Asn Ser Thr Thr Arg Pro Ser Lys
515 520 525

Ser Ser Lys Gly Thr Ser Asn Asn Asn Asn Asn Tyr Asn Asn Phe Asp
530 535 540

Asn Asn Asn Ser Asn Ile Asn Asn Val Asn Asn Lys Ser Val Ser Phe
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Ile Ala Arg Val Asn Ser Thr Gln Ser Leu Arg Ile Arg Gly Leu Glu
 35 40 45

Asn Glu Cys Ala Arg Leu Leu Ser Glu Asn Leu Glu Leu Arg Gly Gln
 50 55 60

Val Leu Arg Leu Glu Lys Glu Leu Gln Asp Asn Ala Ala Arg Arg Val
 65 70 75 80

Ala Asp His Ala Leu Glu Val Lys Ala Lys Met Glu Thr Gln Leu Ala
 85 90 95

Glu Leu Ser Ser Leu Leu Ala Ser Leu Gly Glu Pro Pro Ser Lys Arg
 100 105 110

Arg Leu Ser Glu Glu Arg Arg Tyr Ala Gln Pro Arg Pro Ser Val His
 115 120 125

Arg Ser Pro Pro Leu Arg Arg Ala Arg Gln Glu Ala Asp Gln Glu Leu
 130 135 140

Leu Ala Glu Gln Glu Gly Arg Leu Pro Pro Ile Tyr Glu Asn Lys Thr
 145 150 155 160

Tyr Ala Arg Ala Thr Met Asn Ser Glu Glu Ile Leu Ala Leu Cys Met
 165 170 175

Gln Ala Asp Asp Ser Asn Asp Ser Pro Asp Ile Gly Pro Pro Pro Val
 180 185 190

Ser Arg Phe Val Glu Asp Asp Met Val Ile Pro Cys Ser Pro Ser Pro
 195 200 205

Substitute_Sequence_Listing.TXT

Asn Lys Asn Ala Glu Ala Glu Glu Thr Glu Thr Thr Glu Gln Val Glu
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 Glu Ser Pro Arg Ala Leu Gln Val Pro Pro Ser Leu Ser Pro Pro Lys
 225 230 235 240
 Leu Asp Tyr Asp Arg Arg Pro Asn Met Ile Leu Phe Ser Pro Pro Lys
 245 250 255
 Glu Ser Arg Val Ala Glu Pro Ser Lys Met Phe Ser Pro Pro Met
 260 265 270
 Glu Pro Pro Lys Gln Ser Thr Ser Ala Val Pro Ser Glu Thr Ile Arg
 275 280 285
 Ala Gly Leu Lys Arg Lys Leu Asn Gly Asp Asn Gln Asn Glu Pro Asn
 290 295 300
 Lys Ala Thr Lys Leu Gln Gln Gly Lys Glu Asn Gly Asn Glu Thr Gly
 305 310 315 320
 Ile Lys Lys Gly Leu Ser Ala Arg Asp Pro His Lys Arg Lys Ser Ile
 325 330 335
 Lys Glu Thr Ala Thr Lys Pro Arg Ala Pro Leu Ser Ala Lys Ser Thr
 340 345 350
 Asn Glu His Ile Val Ser Pro Lys Lys Pro Ala Lys Pro His Gln Val
 355 360 365
 Ala Asp Asp Phe Lys Pro Val Lys Val His Lys Ala Ser Lys Gly Lys
 370 375 380
 Glu Lys Val Asp Leu Pro Ala Pro Asp Lys Lys Ser Ala Val Glu Glu
 385 390 395 400
 Thr Gln Gly Asn Ser Thr Ser Ala Phe Thr Lys Val Glu Ile Leu Pro
 405 410 415
 Pro Ala Leu Glu Pro Thr Pro Glu Val Ala Glu Ile Pro Glu Thr Asp
 420 425 430
 Ile Leu Ile Thr Pro Gly Thr Pro Glu Arg Ala Ser Glu Ser Thr Val

Substitute_Sequence_Listing.TXT

435

440

445

Val Thr His Asp Thr Pro Pro Pro Ala His Ile Ser Ser Asn Gly Glu
 450 455 460

Thr Ser Arg Pro Ser Arg Arg Ala Arg Ala Ala Ile Ser Tyr Thr Glu
 465 470 475 480

Pro Asn Leu Arg Asp Lys Met Arg Arg Pro Thr Lys Glu Leu Phe Asp
 485 490 495

Ala Val Ser Gly Glu Gly Lys Phe Leu His Arg Pro Thr Ser Gln Gln
 500 505 510

Gln Gln Gln Gln Arg Lys Gly Asp Glu Ser Ala Pro Thr Ser Val Ser
 515 520 525

Lys Val Lys Val Glu Pro Ser Pro Ala Val Asp Ile Ser Ser Leu Thr
 530 535 540

Ser Ser Ala Leu Phe Glu Lys Glu Lys Glu Lys Glu Pro Gln Pro Asp
 545 550 555 560

Glu Gly Ile Leu Ser Pro Asn Gly Ile Leu Pro Ser Ser Val Asp Leu
 565 570 575

Gly Arg Arg Arg Arg Ala Ser Ser Phe Ser Thr Ala Ala Pro Ala Met
 580 585 590

Thr Ile Pro Ser Val Gln Glu Gln Ser Thr Leu Asn Leu Pro Ala Ala
 595 600 605

Asp Glu Thr Asp Glu Asn Ala Ala Val Glu Ala Gln Ile Gln Lys Glu
 610 615 620

Leu Ser Asn Ser Ile Thr Thr Arg Pro Arg Gly Gly Lys Gly Arg Gln
 625 630 635 640

Ser Met Ser Arg Ser Val Pro Thr Ile Pro Thr Glu Asn Tyr Glu His
 645 650 655

Glu Asp Ala Gln Leu Ser Thr Asn Ser Ala Ser Val Asp Leu Tyr Asp
 660 665 670

Phe Ala Ser Cys Ala Ser Pro Asp Ser Ala Ala Pro Gln Leu Glu Ala
 675 680 685

Substitute_Sequence_Listing.TXT

Thr Thr Gly Asp Val Pro Val Asn Lys Lys Ala Pro Lys Gly Ser Arg
690 695 700

Arg Ala Ser Ser Ala Ala Ser Thr Glu Thr Thr Ala Thr Ala Ser Ala
705 710 715 720

Lys Pro Arg Ser Ser Arg Lys Arg Ala Ser Met Leu Val Pro Lys Lys
725 730 735

Ser Leu Trp Ala Glu Glu Leu Ala Gln Glu Glu Glu Asp Glu Glu Asp
740 745 750

Val Gly Asn Asp Ser Gly Gly Ser Leu Ser Lys Gly Arg Ala Ser Arg
755 760 765

Arg Arg Ser Met Met Leu
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<211> 1671
<212> DNA
<213> Arabidopsis thaliana

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gaagacaaca ttgacaaca gaagttggtc tctgatagtg acaatgatgc tgaaccat 720
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actcgagaag ccagccaaac agaaacctt caaaagggtg ttgacgcaa agaaattaag 840
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Substitute_Sequence_Listing.TXT

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aggtcggcaa taaggtctgc tatgtttaat atccaagagc tgggcgttat tcaaaacttg 1080
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<210> 10
<211> 556
<212> PRT
<213> Arabidopsis thaliana
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<400> 10
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20 25 30
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Met Asn Ser Ala Gln Arg Arg Lys Leu Gly Asp Ile Thr Asn Leu Gln
35 40 45
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Asn Gln Lys Asn Leu Met Asn Gln Gly Ala Lys His Gln Gln Gln Ala
50 55 60
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Ile Leu Ile Ser Ser Lys Glu Asn Ala Glu Asn Leu Gln Lys Ala Leu
65 70 75 80
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Arg Asn Ser Ser Glu Asn Thr Lys Leu Met Lys Val Val Met Glu Arg
85 90 95
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Asp Gly Ile Lys Ser Asp Leu Lys Lys Leu Arg Ile Glu Phe Gln Lys
100 105 110
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Substitute_Sequence_Listing.TXT

Val Gln Glu Gln Asn Leu Leu Ala Gln Ala Asn Thr Arg Ile Leu
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 Ala Leu Lys Val Leu Gln His Glu Leu Gly Cys Lys Asn Gly Leu Val
 130 135 140
 Met Ala Arg Lys Met Leu Leu Lys Ala Gln Ala Asn Ala Cys Gly Gly
 145 150 155 160
 Ala Cys Lys Thr Phe Gln Pro Asn Asp Ala Asp His Glu His Ala Ser
 165 170 175
 Gly Ser Ser Asn Ala Asn Ser Leu Gln Arg Asn Glu Lys Ala Asn Ser
 180 185 190
 Lys Arg Arg Val Ser Gly Arg Lys Asn Pro Ala Asn Ser Glu Val Leu
 195 200 205
 Asp Ile Ile Gly Arg Ser Gly Glu Thr Cys Gln Met Glu Asp Asn Ile
 210 215 220
 Asp Asn Lys Lys Leu Val Ser Asp Ser Asp Asn Asp Ala Glu Asn His
 225 230 235 240
 Ile Asn Asp Asn Val Gln Ser Lys Arg Tyr Cys Ala Gly Arg Gln Ser
 245 250 255
 Ser Ser Ser Lys Thr Arg Glu Ala Ser Gln Thr Glu Thr Leu Gln Lys
 260 265 270
 Val Val Asp Ala Lys Glu Ile Lys Gly Asp Ala Arg Phe Ser Leu Thr
 275 280 285
 Lys His Ser Asp Trp Leu Lys Ser Gln Glu Pro Glu Pro Ser Glu Ser
 290 295 300
 Leu Tyr Glu Ser Arg Phe Pro Leu Arg Arg Arg Ser Ala Arg Leu Lys
 305 310 315 320
 Ser Gln Glu Pro Glu Pro Ser Glu Ser Phe His Asp Ser Ile Glu Thr
 325 330 335
 Thr Lys Arg Arg Arg Ser Ala Ile Arg Ser Ala Met Phe Asn Ile Gln
 340 345 350

Substitute_Sequence_Listing.TXT

Glu Leu Gly Val Ile Gln Asn Leu Asn Gly Leu Pro Asp Asp Gln Glu
355 360 365

Ile Ala Ala Lys Ala Arg Cys Ser Ala Arg Glu Gln Ser Thr Gly Ser
370 375 380

Lys Pro Glu Ala Val Glu Pro His Asp Thr Lys Glu Ile Ile Gly Lys
385 390 395 400

Ser Arg Ile Ser Leu Arg Arg Gln Ser Ala Arg Phe Asn Phe Gln Glu
405 410 415

Leu Gly Val Thr Glu Asn Leu Asn Gly Pro His Asp Asp Gln Thr Ile
420 425 430

Ala Ala Asn Ala Arg Cys Cys Ala Ser Glu Gln Ser Ile Gly Ser Lys
435 440 445

Pro Glu Ala Val Glu Pro His Asp Ile Glu Glu Arg Ile Gly Lys Ile
450 455 460

Arg Val Ser Ser Arg Arg Gln Ser Ala Asn Ile Glu Thr Pro Arg Ala
465 470 475 480

Ile Lys Glu Pro Ala Asn Pro Pro Leu His Asp Asp Asn Val Glu Glu
485 490 495

Ser Ser Gln Ile Ser Cys Ser Val Ser Met Glu Leu Lys Arg Glu Ser
500 505 510

Lys Lys Lys Pro Thr Gly Asp Glu Ser Glu Glu Met Arg Lys Thr Thr
515 520 525

Val Gly Arg Pro Ser Arg Gln Ala Ala Glu Lys Ile Lys Ser Tyr Lys
530 535 540

Glu Pro Ser Leu Lys Glu Lys Met Arg Gly Gly Phe
545 550 555

<210> 11
<211> 1341

<212> DNA
<213> Arabidopsis thaliana

<400> 11
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Substitute_Sequence_Listing.TXT

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ttagcgctca aggatctcca gcatagaactt ggctgcaaga atgctttact taaagtcaag	300
aaacatcttg aggagcaagt acttccacgt acacatcatg aatcgaaaga caaggtttca	360
gcaagcgctt ctgattggga ttgcaaatcc tttcaggtgc atgacataaa acataaagat	420
accaagagaa agcgaacaac aaggataaaa tcttcagtaa gtgccgacgt caagccaata	480
cctgtgaatg attctaacag taaagctaac cgtaaaagaa gagtttctgg agtaatagat	540
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tctcgagggg taaaccaaga tattgacaat gttgtcaaca agaagtttgt tcctgatgca	660
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agatttgatg ttcaagaaac taaacaaacg gaaaagttgc ttgagatgga tggtgccaaa	780
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tcaaaggata agcctaaagc tgatgaaaac gaagggatga caagaagatc atctgtggga	1260
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<210> 12
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 <212> PRT
 <213> Arabidopsis thaliana

<400> 12

Met Asp Lys Glu Glu Thr Gln Gln Lys Glu Asn Met Leu Phe Ser Ser
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Gln Glu Tyr Ala Ala Lys Leu Gln Lys Ala Phe Pro Leu His Phe Asn
 20 25 30

Leu Glu Asn Met Thr Leu Met Lys Ala Leu Ala His Arg Asn Lys Leu
 35 40 45

Substitute_Sequence_Listing.TXT

Val Glu Leu Ser Gly Ile Glu Ile Gln Lys Leu Arg Ile Asn Leu Arg
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Ser Val Gln Glu Lys Asn Leu Gln Leu Ala Gln Ala Asn Ser Gln Met
65 70 75 80

Leu Ala Leu Lys Asp Leu Gln His Glu Leu Gly Cys Lys Asn Ala Leu
85 90 95

Leu Lys Val Lys Lys His Leu Glu Glu Gln Val Leu Pro Arg Thr His
100 105 110

His Glu Ser Lys Asp Lys Val Ser Ala Ser Ala Ser Asp Gly Asp Cys
115 120 125

Lys Ser Phe Gln Val His Asp Ile Lys His Lys Asp Thr Lys Arg Lys
130 135 140

Arg Thr Thr Arg Ile Lys Ser Ser Val Ser Ala Asp Val Lys Pro Ile
145 150 155 160

Pro Val Asn Asp Ser Asn Ser Lys Ala Asn Arg Lys Arg Arg Val Ser
165 170 175

Gly Val Ile Asp Thr Thr Gly Ile Pro Glu Glu Ile Cys Gln Thr Glu
180 185 190

Asp Asp Ile Asp Lys Gly Val Val Ser Arg Gly Val Asn Gln Asp Ile
195 200 205

Asp Asn Val Val Asn Lys Lys Phe Val Pro Asp Ala Ala Asn Pro Val
210 215 220

Lys Glu Ser Val His Arg Lys Arg Gln Cys Thr Arg Arg Gln Ser Thr
225 230 235 240

Arg Phe Asp Val Gln Glu Thr Lys Gln Thr Glu Lys Leu Glu Met
245 250 255

Asp Gly Ala Lys Glu Ser Lys Glu Thr Ala Ser Phe Ser Leu Arg Arg
260 265 270

Arg Ser Ala Arg Leu Arg His Glu Glu Ala Glu Pro Cys Lys Ser Leu
275 280 285

His Glu Gly Asp Glu Val Arg Glu Thr Ile Lys Arg Arg Arg Val Ser
290 295 300

Substitute_Sequence_Listing.TXT

Leu Arg Leu Ser Ala Arg Phe Asp Ile Gln Glu Pro His Val Thr Glu
305 310 315 320

Thr Ser Asn Ala Asp Asp Ala Arg Ser Ile Val Ile Glu Glu Ser Ala
325 330 335

Gly Ser Arg Ser Glu Ser Val Glu Pro Ser Glu Ser Arg His Glu Thr
340 345 350

Lys Glu Ile Thr Arg Lys Arg Ser Phe Ser Thr Arg Arg Gln Ser Thr
355 360 365

Lys Gly Lys Ser Gln Thr Asp Glu Ala Ile Lys Glu Ile Ala Thr Asp
370 375 380

Pro Ser Leu Val Asn Thr Ile Val Gln Glu Cys Asp Gln Glu Thr Glu
385 390 395 400

Ser Lys Asp Lys Pro Lys Ala Asp Glu Asn Glu Gly Met Thr Arg Arg
405 410 415

Ser Ser Val Gly Arg Pro Ser Arg His Ala Ala Glu Lys Val Gln Ser
420 425 430

Tyr Arg Glu Val Ser Leu Arg Val Lys Met Arg Arg Lys Cys
435 440 445

<210> 13
<211> 1554
<212> DNA
<213> mouse

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gttgaccagg gccaaagtacc cactaacact gctacactac tgagatatta ccaagataac 180
aacaggttgt tagtcttggc tttggaaaat gagaaatcca aagtgagaga agcacaggat 240
gtcatcctgc aactgagaaa agaattgtac taccttactt gtcagctgta tgcattgaaa 300
gagaagctaa cttcccgaca aagtgaagaa actactcaga actggaaagg acgtccctca 360
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ccagagacac agggttgcga ttttgattca ggtaaaagtg agtctactga tgaagtctta 540
cccagaacta tatctatccg tcgccattta aggaagatt ttagtaatat aagccactcc 600

Substitute_Sequence_Listing.TXT

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aaaatgaaca	atggctgcaa	caaagaaacg	gatagcagca	actcagaagt	gagtgcctc	1080
gaatgcagta	cctctgagga	tgagtctgat	gacctctacc	tgctccctc	caagcgcttg	1140
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 <211> 517
 <212> PRT
 <213> mosue

<400> 14

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Asp Ile Lys Asn Arg Met Lys Glu Lys Arg Asn Lys Asn Leu Ala Gly
 20 25 30

Ile Gly Lys Arg Lys Ser Phe Ile Val Ala Pro Gly Gln Val Pro Thr
 35 40 45

Asn Thr Ala Thr Leu Leu Arg Tyr Tyr Gln Asp Asn Asn Arg Leu Leu
 50 55 60

Val Leu Ala Leu Glu Asn Glu Lys Ser Lys Val Arg Glu Ala Gln Asp
 65 70 75 80

Val Ile Leu Gln Leu Arg Lys Glu Cys Tyr Tyr Leu Thr Cys Gln Leu

Substitute_Sequence_Listing.TXT

85

90

95

Tyr Ala Leu Lys Glu Lys Leu Thr Ser Arg Gln Ser Glu Glu Thr Thr
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 Gln Asn Trp Lys Gly Arg Pro Ser Asp Val Val Ser Ser Ile Asp Asn
 115 120 125
 Thr Thr Arg Asp Leu Ser Gly Lys Ser Leu Gln Gln Ile Ala Val Glu
 130 135 140
 Glu Thr Asp Cys Pro Tyr Gln Thr Thr Glu Pro Ser Pro Ala Val Thr
 145 150 155 160
 Pro Glu Thr Gln Gly Cys Asp Phe Asp Ser Gly Lys Val Glu Ser Thr
 165 170 175
 Asp Glu Val Leu Pro Arg Thr Ile Ser Ile Arg Arg His Leu Arg Lys
 180 185 190
 Asp Phe Ser Asn Ile Ser His Ser Thr Thr Leu Glu Asp Cys Lys Ala
 195 200 205
 Ser Pro Arg Val Ala Gln Ser Leu Glu Val Lys Gly Ser Arg Cys Arg
 210 215 220
 Glu Val Thr Val Thr Leu His Arg Leu Glu Asn Val Cys Leu Trp Asn
 225 230 235 240
 Lys Asp Gln Ile Ser Leu Cys Ser Arg Leu Ile Asn Pro Ala Lys Ile
 245 250 255
 Thr Glu Thr Glu Val Ile Leu Ser Ser Lys Pro Glu Gln Ile Glu Ser
 260 265 270
 Lys His Lys Arg Ala Arg Lys Arg Arg Ala Glu Gln Arg Arg Thr Lys
 275 280 285
 Gln Arg Cys Lys Ser Lys Ser Ser Leu Arg Ser Lys Gly Asn Lys Asn
 290 295 300
 Lys Asp Lys Gln Gly Leu Pro Pro Thr Thr Leu Asp Gly Gly Ile Gly
 305 310 315 320
 Ser Cys Asp Ala Tyr Asp Phe Asn Leu Lys Gly Thr Val His Pro Thr
 325 330 335

Substitute_Sequence_Listing.TXT

Pro Phe Arg Gln Lys Met Asn Asn Gly Cys Asn Lys Glu Thr Asp Ser
340 345 350

Ser Asn Ser Glu Val Ser Asp Leu Glu Cys Ser Thr Ser Glu Asp Glu
355 360 365

Ser Asp Asp Leu Tyr Leu Pro Pro Ser Lys Arg Leu Arg Asp Tyr Arg
370 375 380

Glu Ser Glu Arg Ala Val Thr Arg Pro Arg Ser Lys Arg Gly Leu Gln
385 390 395 400

Tyr Pro Asp Gly Lys Glu Arg Lys Glu Val Leu Pro Ser Thr Ala Pro
405 410 415

Thr Gly Ile Pro Pro Glu Thr Gln Glu Ser Pro Arg Cys Ser Leu Lys
420 425 430

Asp Val Thr Asn Ile Leu Gln Cys Pro Arg Val Lys Ile Arg Lys Pro
435 440 445

Ser Leu Pro Pro Lys Arg Arg Glu Asp Ser Pro Ala Val Ala Leu Thr
450 455 460

Lys Arg Arg Cys Ser Thr Ile Lys Ser Tyr Lys Glu Pro Thr Leu Ala
465 470 475 480

Ser Lys Leu Arg Arg Gly Asp Pro Phe Thr Asp Leu Cys Phe Leu Asn
485 490 495

Ser Pro Ile Phe Lys Gln Lys Arg Gly Met Arg Cys Pro Lys Arg Arg
500 505 510

Thr Lys Gln Thr Gln
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<210> 15
<211> 3495
<212> DNA
<213> mouse

<400> 15
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gcccttagta aagagaaga gaattctcga agaattacta ccgaaaagat gcaattacag 240
aaagaagtag agaaactgaa ttttgagaat acctttcttc gcttaaagtt aaataccttg 300

Substitute_Sequence_Listing.TXT

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gaaaaagaca	actttccctt	tcatacccaa	gcaataaag	aaaccaccag	tggaaaccta	1920
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gactgtaaga	cccagaatgt	tctggatctg	cacaagcaaa	ttcctgatct	ataccctgat	2040
cggaatgagt	cccagattag	caaaatccct	aggcaaaaag	taaatcgcaa	gacagaagta	2100
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Substitute_Sequence_Listing.TXT

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 <212> PRT
 <213> mouse

<400> 16

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Ala Ser Lys Ile Lys Ala Lys Ile Leu Asn Asn Ser Ser Ile Phe Lys

Substitute_Sequence_Listing.TXT

35

40

45

Ile Ser Leu Lys His Asn Asn Arg Ala Leu Ala Arg Ala Leu Ser Lys
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 Glu Lys Glu Asn Ser Arg Arg Ile Thr Thr Glu Lys Met Gln Leu Gln
 65 70 75 80
 Lys Glu Val Glu Lys Leu Asn Phe Glu Asn Thr Phe Leu Arg Leu Lys
 85 90 95
 Leu Asn Thr Leu Asn Lys Lys Leu Val Glu Ile Glu Ser His Val Ser
 100 105 110
 Asn Asp Leu Leu Thr Ala Ile Glu Ile Ser Ser Leu Ser Glu Phe His
 115 120 125
 Gln Gly Ser Phe Leu Leu Ser Ala Thr Lys Lys Gln Arg Asn Ser Lys
 130 135 140
 Gln Cys Lys Pro Ala His Leu Pro Tyr Ala Arg Val Leu Leu Thr Ser
 145 150 155 160
 Glu Asn Asp Asp Asp Gly Ala Asp Asp Lys Trp Gln Thr Lys Cys
 165 170 175
 Asn Asn Arg Thr Ile Ser Lys Thr Ser Pro Asp Ser Thr Ser Ser Val
 180 185 190
 Ser Arg Gln Pro Ser Ser Leu His Gln Cys Asn Leu Lys Ala Phe Pro
 195 200 205
 Pro Lys Glu Asp Asn Gln Lys Thr Cys Gly Ser Gly His Leu Glu His
 210 215 220
 Thr Ser Ser Val Asp Ile Leu Pro Asn Glu Ser His Ser Asp Gln Ser
 225 230 235 240
 Pro Lys Ser Ser Leu Ser Glu Met Lys Thr Ala Pro Ser Pro Ser Leu
 245 250 255
 Arg Arg Glu Lys Leu Ser His Gly Asn Val Thr Met Arg Lys Lys Cys
 260 265 270
 Val Ser Ser Thr Pro Asp Ile Leu Tyr Val Thr Asp Leu Asp His Gln
 275 280 285

Substitute_Sequence_Listing.TXT

Pro Thr Ser Ser Pro Gly Ser Asn Trp Asn Asn Glu Ile His Gly His
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Thr Asn Glu Thr Ser Asn Asn Thr Gln Arg Asn Ala Glu Cys Phe Leu
 305 310 315

Asp Leu Pro Ser Glu Ser Ser Ser Glu Pro Asp Ala Lys Arg Met Glu
 325 330 335

Leu Val Gln Lys Asn Thr Asp Ser Phe His Phe Gln Lys Thr Val Tyr
 340 345 350

Asp Ala Ala Asp Met Glu Leu Thr Ala Thr Asp Ile Gly Lys Ile Val
 355 360 365

Ala Val Ser Lys Ser Lys Lys Asn Gln Asn Lys Lys Lys Ala Asp Cys
 370 375 380

Arg Lys Glu Thr Phe Arg Lys Val Lys Gly Ala Ser Ser Asp Lys Lys
 385 390 395 400

Arg Glu Ser Ser Lys Arg Glu Cys Lys Asp Gly Ser Glu Val Gly Ala
 405 410 415

Glu Glu Glu Ala Asp Ala Ala Arg Ala Glu Arg Gly Ala Gly Val Leu
 420 425 430

Asp Gly Arg Gly Asp Ser Glu Glu Pro Asn Cys Ile Ser Ser Thr Glu
 435 440 445

Gln Pro Ser Gln Val Asn Thr Gln Lys Lys Arg Thr Leu Gln Asn Ser
 450 455 460

Ser Asp Gln Glu Asn Ile Gln Asn Thr Lys Arg Arg Gln Thr Tyr Thr
 465 470 475 480

Thr Asp Glu Gln Glu Thr Asn Pro Phe Ser Arg His Ser Val Lys
 485 490 495

Phe Leu Gln Asp Gly Lys Phe Asp Leu Cys Gln Lys Thr Leu His His
 500 505 510

Asn Leu Ser Lys Pro Ser Arg Gln Thr Phe Val Ile Arg Lys Ser Glu
 515 520 525

Lys Asp Asn Leu Phe Pro Asn Gln Glu Asp Lys Asp Thr Ile Ser Glu
 530 535 540

Substitute_Sequence_Listing.TXT

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 580 585 590
 Lys Gln Lys Ile Asn Arg Arg Thr Lys Ile Ile Ser Val Met Ser Gln
 595 600 605
 Val Tyr Glu Asp Asn Asp Lys Asp Ile His Val Leu Glu Lys Asp Asn
 610 615 620
 Phe Pro Phe His Thr Gln Ala Asn Lys Glu Thr Thr Ser Gly Asn Leu
 625 630 635 640
 Glu Ser Ser Lys Glu Phe Glu Ser Pro Leu Leu Phe Thr Arg Asp Asn
 645 650 655
 Gly Ser Leu Arg Asp Cys Lys Thr Gln Asn Val Leu Asp Leu His Lys
 660 665 670
 Gln Ile Pro Asp Leu Tyr Pro Asp Arg Asn Glu Ser Gln Ile Ser Lys
 675 680 685
 Ile Pro Arg Gln Lys Val Asn Arg Lys Thr Glu Val Ile Ser Gly Val
 690 695 700
 Lys Cys Phe Ser Asn Asp Gln Gly Val His Cys Ser Glu Lys Asp Lys
 705 710 715 720
 Ser Leu Leu Leu Gln Lys Asp Lys Asp Phe Pro Gly Thr Leu Lys Asp
 725 730 735
 Leu Ser Glu Phe Asp Thr Pro Ala Phe Cys Asn Lys Asp Ser Ala Lys
 740 745 750
 Ser Cys Asp Tyr Lys Ser Glu Met Leu Leu Gly Leu Lys Lys His Asp
 755 760 765
 Pro Asn Met Gln Pro Ala Cys Gln Asp Asp Ser Lys Ala Gly Lys Lys
 770 775 780
 Leu Arg Gln Lys Val Asn Arg Lys Thr Glu Ile Ile Ser Lys Ile Thr
 785 790 795 800

Substitute_Sequence_Listing.TXT

Gln Ile His Glu Asn Asp Arg Gly Ser Thr His Asp Ser Leu Asn Lys
 805 810 815
 Lys Leu Cys Gln Lys Val Asn Ile Ser Lys Ile Ile Ser Gln Met Asn
 820 825 830
 Gln Ile Tyr Glu Thr Ile Asn Glu Asp Gly Asn Gly Phe Lys Ser Ser
 835 840 845
 Ile Lys Asp Cys Glu Asp Ile Lys Ser Cys Asp Phe Gly Glu Ile Asn
 850 855 860
 Ser Asn Lys Lys Glu Asn Tyr Asp Pro Ile Gln Asp Pro Cys Thr Leu
 865 870 875 880
 Val Lys Lys Thr Lys Arg Lys Gly Ser Cys Lys Ala Gly Ser Ser Leu
 885 890 895
 Ala Gly Ala Lys Asn Arg Cys Gly Leu Gln Leu Thr Asp Ser Ser Gln
 900 905 910
 Val Gln Ser Val Pro Leu Asp Ser Gly Leu Arg His His Pro Asn Glu
 915 920 925
 Ala Asp Ser Gly Pro Gly Glu Gln Thr Asn Leu Pro Lys Met Gln Lys
 930 935 940
 Gln Ser Ala Gly Arg Ser Leu Gly Asp Ala Phe Ser Val Ser Leu Gly
 945 950 955 960
 Lys Glu Gly Ser Arg Pro Ala Lys Ala Val Ser Lys Met Thr Pro Lys
 965 970 975
 Ser Lys Lys Arg Lys Leu Pro Leu Gly Cys Ser Pro Glu Thr His Gly
 980 985 990
 Thr Val Glu Ile Thr Pro Asn Thr Asp Leu Ala Lys Ala Val Asp Ser
 995 1000 1005
 Gln Gln Thr Glu Lys Glu Asn Tyr Leu Glu Lys Glu Lys Ile Ala
 1010 1015 1020
 Lys Arg Lys Pro Asp Phe Cys Thr Lys Val Leu Lys Pro Leu Ser
 1025 1030 1035
 Glu Thr Cys Ser Ser Asn Ile Lys Asn Ser Ser Leu Asp Ser Met

Substitute_Sequence_Listing.TXT
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1040

Cys Lys Ser Ser Leu Pro Leu Ser Ile Ser Ser Arg Lys Thr Leu
1055 1060
Met Leu Glu Glu Ser Ser Ser Leu Glu Ser Thr Cys Ile Phe Gln
1070 1075 1080
Val Gly Asp Ala Ala His Glu Lys Ile Thr Thr Gly Thr Arg Asn
1085 1090 1095
Pro His His Arg Thr Gln Lys Ser Thr Pro Gly Ser Arg Thr Ser
1100 1110
Leu Val Leu Val Asp Thr Ser Ser Val Ser Asp Thr Asn Pro Ala
1115 1120 1125
Asn Pro Glu Asn Glu Ser Glu Gly Gln Ser Ser His Pro Met Arg
1130 1135 1140
Arg Lys Arg Gln Cys Val Pro Leu Asn Leu Thr Glu Pro Ser Leu
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Arg Ser Lys Met Arg Arg
1160

<210> 17
<211> 1584
<212> DNA
<213> Homo sapiens

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gctgcaccat gccaaataat caccaacact tctacactgc tgaaaaatta ccaagacaac 180
aacaaaatgt tagtttttagc ttgggaaat gaaaaatcca aagtgaaga agccaagat 240
atcatcctac agctgagaaa agaattgtac tatctcacat gtcagctata tgcattgaaa 300
ggaaaactta catcacaaca aacagtagaa cctgctcaga accaggaaat atgttcctct 360
ggaatggacc ccaatagtga tgacagctcc agaaatttat ttgtgaagga ttaccgcaa 420
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atacctacta ttctcaaga cactggga gttgatttg attcagggtga agctaagtct 540
actgataatg tcttacctag aactgtatct gttcgtagca gtttaaagaa acattgtaac 600
agtatatgtc agtttgatag cttggatgat ttgaaacca gtcatttggc agggaagtct 660

Substitute_Sequence_Listing.TXT

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cagccaggaa cgtttactaa aacaaaagaa gacatttttag aatctaaatc tgaacaaaat	840
aaaagtaagc aaagagatatac acaagaaaga aaaagagaag agaaaagaaa agctaacagg	900
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<210> 18
 <211> 527
 <212> PRT
 <213> Homo sapiens

<400> 18

Met Ala Lys Glu Arg Cys Leu Lys Lys Ser Phe Gln Asp Ser Leu Glu
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Asp Ile Lys Lys Arg Met Lys Glu Lys Arg Asn Lys Asn Leu Ala Glu
 20 25 30

Ile Gly Lys Lys Arg Arg Ser Phe Ile Ala Ala Pro Cys Gln Ile Ile Thr
 35 40 45

Asn Thr Ser Thr Leu Leu Lys Asn Tyr Gln Asp Asn Asn Lys Met Leu
 50 55 60

Val Leu Ala Leu Glu Asn Glu Lys Ser Lys Val Lys Glu Ala Gln Asp
 65 70 75 80

Ile Ile Leu Gln Leu Arg Lys Glu Cys Tyr Tyr Leu Thr Cys Gln Leu
 85 90 95

Substitute_Sequence_Listing.TXT

Tyr Ala Leu Lys Gly Lys Leu Thr Ser Gln Gln Thr Val Glu Pro Ala
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 Gln Asn Gln Glu Ile Cys Ser Ser Gly Met Asp Pro Asn Ser Asp Asp
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 Ser Ser Arg Asn Leu Phe Val Lys Asp Leu Pro Gln Ile Pro Leu Glu
 130 135 140
 Glu Thr Glu Leu Pro Gly Gln Gly Glu Ser Phe Gln Ile Glu Asp Gln
 145 150 155 160
 Ile Pro Thr Ile Pro Gln Asp Thr Leu Gly Val Asp Phe Asp Ser Gly
 165 170 175
 Glu Ala Lys Ser Thr Asp Asn Val Leu Pro Arg Thr Val Ser Val Arg
 180 185 190
 Ser Ser Leu Lys Lys His Cys Asn Ser Ile Cys Gln Phe Asp Ser Leu
 195 200 205
 Asp Asp Phe Glu Thr Ser His Leu Ala Gly Lys Ser Phe Glu Phe Glu
 210 215 220
 Arg Val Gly Phe Leu Asp Pro Leu Val Asn Met His Ile Pro Glu Asn
 225 230 235 240
 Val Gln His Asn Ala Cys Gln Trp Ser Lys Asp Gln Val Asn Leu Ser
 245 250 255
 Pro Lys Leu Ile Gln Pro Gly Thr Phe Thr Lys Thr Lys Glu Asp Ile
 260 265 270
 Leu Glu Ser Lys Ser Glu Gln Thr Lys Ser Lys Gln Arg Asp Thr Gln
 275 280 285
 Glu Arg Lys Arg Glu Glu Lys Arg Lys Ala Asn Arg Arg Lys Ser Lys
 290 295 300
 Arg Met Ser Lys Tyr Lys Glu Asn Lys Ser Glu Asn Lys Lys Thr Val
 305 310 315 320
 Pro Gln Lys Lys Met His Lys Ser Val Ser Ser Asn Asp Ala Tyr Asn
 325 330 335
 Phe Asn Leu Glu Glu Gly Val His Leu Thr Pro Phe Arg Gln Lys Val
 340 345 350

Substitute_Sequence_Listing.TXT

Ser Asn Asp Ser Asn Arg Glu Glu Asn Asn Glu Ser Glu Val Ser Leu
355 360 365

Cys Glu Ser Ser Gly Ser Gly Asp Asp Ser Asp Asp Leu Tyr Leu Pro
370 375 380

Thr Cys Lys Tyr Ile Gln Asn Pro Thr Ser Asn Ser Asp Arg Pro Val
385 390 395 400

Thr Arg Pro Leu Ala Lys Arg Ala Leu Lys Tyr Thr Asp Glu Lys Glu
405 410 415

Thr Glu Gly Ser Lys Pro Thr Lys Thr Pro Thr Thr Thr Pro Pro Glu
420 425 430

Thr Gln Gln Ser Pro His Leu Ser Leu Lys Asp Ile Thr Asn Val Ser
435 440 445

Leu Tyr Pro Val Val Lys Ile Arg Arg Leu Ser Leu Ser Pro Lys Lys
450 455 460

Asn Lys Ala Ser Pro Ala Val Ala Leu Pro Lys Arg Arg Cys Thr Ala
465 470 475 480

Ser Val Asn Tyr Lys Glu Pro Thr Leu Ala Ser Lys Leu Arg Arg Gly
485 490 495

Asp Pro Phe Thr Asp Leu Cys Phe Leu Asn Ser Pro Ile Phe Lys Gln
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Lys Lys Asp Leu Arg Arg Ser Lys Lys Ser Met Lys Gln Ile Gln
515 520 525

<210> 19

<211> 3798

<212> DNA

<213> Homo sapiens

<400> 19

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ctattgcaaa aagaagtaga gaaactgaat ttgagaaca catttcttcg cctaaagcta 300

aataacttga ataagaagct tatagacata gaagctctca tgaacaataa cttgataact 360

Substitute_Sequence_Listing.TXT

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gttcagcaaa	atgaatcaaa	agttaataag	aagcttaggc	agaaagtaaa	tcggaagaca	2160
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Substitute_Sequence_Listing.TXT

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gaacggacaa	gcagaagaag	aaggtgtact	ctttcttatt	ttaaagagcc	aagcctcaga	3780
gacaagatga	gaagatga					3798

<210> 20
 <211> 1265
 <212> PRT
 <213> Homo sapiens
 <400> 20

Met Glu Cys Pro Val Met Glu Thr Gly Ser Leu Phe Thr Ser Gly Ile

Substitute_Sequence_Listing.TXT

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 Val Ser Leu Ala Ser Lys Ile Lys Thr Lys Ile Leu Asn Asn Ser Ser
 35 40 45
 Ile Phe Lys Ile Ser Leu Lys His Asn Asn Arg Ala Leu Ala Gln Ala
 50 55 60
 Leu Ser Arg Glu Lys Glu Asn Ser Arg Arg Ile Thr Thr Glu Lys Met
 65 70 75 80
 Leu Leu Gln Lys Glu Val Glu Lys Leu Asn Phe Glu Asn Thr Phe Leu
 85 90 95
 Arg Leu Lys Leu Asn Asn Leu Asn Lys Lys Leu Ile Asp Ile Glu Ala
 100 105 110
 Leu Met Asn Asn Asn Leu Ile Thr Ala Ile Glu Met Ser Ser Leu Ser
 115 120 125
 Glu Phe His Gln Ser Ser Phe Leu Leu Ser Ala Ser Lys Lys Lys Arg
 130 135 140
 Ile Ser Lys Gln Cys Lys Leu Met Arg Leu Pro Phe Ala Arg Val Pro
 145 150 155 160
 Leu Thr Ser Asn Asp Asp Glu Asp Glu Asp Lys Glu Lys Met Gln Cys
 165 170 175
 Asp Asn Asn Ile Lys Ser Lys Thr Leu Pro Asp Ile Pro Ser Ser Gly
 180 185 190
 Arg Thr Thr Gln Pro Leu Ser Thr Gln Asp Asn Ser Gly Val Leu Phe
 195 200 205
 Leu Lys Glu Asn Asn Gln His Val Tyr Gly Leu Asp Asp Ser Glu His
 210 215 220
 Ile Ser Ser Ile Val Asp Val Pro Pro Arg Glu Ser His Ser His Ser
 225 230 235 240
 Asp Gln Ser Ser Lys Thr Ser Leu Met Ser Glu Met Arg Asn Ala Gln
 245 250 255

Substitute_Sequence_Listing.TXT

Ser Ile Gly Arg Arg Trp Glu Lys Pro Ser Pro Ser Asn Val Thr Glu
260 265 270

Arg Lys Lys Arg Gly Ser Ser Trp Glu Ser Asn Asn Leu Ser Ala Asp
275 280 285

Thr Pro Cys Ala Thr Val Leu Asp Lys Gln His Ile Ser Ser Pro Glu
290 295 300

Leu Asn Cys Asn Asn Glu Ile Asn Gly His Thr Asn Glu Thr Asn Thr
305 310 315 320

Glu Met Gln Arg Asn Lys Gln Asp Leu Pro Gly Leu Ser Ser Glu Ser
325 330 335

Ala Arg Glu Pro Asn Ala Glu Cys Met Asn Gln Ile Glu Asp Asn Asp
340 345 350

Asp Phe Gln Leu Gln Lys Thr Val Tyr Asp Ala Asp Met Asp Leu Thr
355 360 365

Ala Ser Glu Val Ser Lys Ile Val Thr Val Ser Thr Gly Ile Lys Lys
370 375 380

Lys Ser Asn Lys Lys Thr Asn Glu His Gly Met Lys Thr Phe Arg Lys
385 390 395 400

Val Lys Asp Ser Ser Ser Glu Lys Lys Arg Glu Arg Ser Lys Arg Gln
405 410 415

Phe Lys Asn Ser Ser Asp Val Asp Ile Gly Glu Lys Ile Glu Asn Arg
420 425 430

Thr Glu Arg Ser Asp Val Leu Asp Gly Lys Arg Gly Ala Glu Asp Pro
435 440 445

Gly Leu Phe Phe Asn Asn Glu Gln Leu Ala Gln Met Asn Glu Gln Leu
450 455 460

Ala Gln Val Asn Glu Leu Lys Lys Met Thr Leu Gln Thr Gly Phe Glu
465 470 475 480

Gln Gly Asp Arg Glu Asn Val Leu Cys Asn Lys Lys Glu Lys Arg Val
485 490 495

Thr Asn Glu Gln Glu Glu Thr Tyr Ser Leu Ser Gln Ser Ser Gly Lys
500 505 510

Substitute_Sequence_Listing.TXT

Phe His Gln Glu Ser Lys Phe Asp Lys Gly Gln Asn Ser Leu Thr Cys
 515 520 525
 Asn Lys Ser Lys Ala Ser Arg Gln Thr Phe Val Ile His Lys Leu Glu
 530 535 540
 Lys Asp Asn Leu Leu Pro Asn Gln Lys Asp Lys Val Thr Ile Tyr Glu
 545 550 555 560
 Asn Leu Asp Val Thr Asn Glu Phe His Thr Ala Asn Leu Ser Thr Lys
 565 570 575
 Asp Asn Gly Asn Leu Cys Asp Tyr Gly Thr His Asn Ile Leu Asp Leu
 580 585 590
 Lys Lys Tyr Val Thr Asp Ile Gln Pro Ser Glu Gln Asn Glu Ser Asn
 595 600 605
 Ile Asn Lys Leu Arg Lys Lys Val Asn Arg Lys Thr Glu Ile Ile Ser
 610 615 620
 Gly Met Asn His Met Tyr Glu Asp Asn Asp Lys Asp Val Val His Gly
 625 630 635 640
 Leu Lys Lys Gly Asn Phe Phe Phe Lys Thr Gln Glu Asp Lys Glu Pro
 645 650 655
 Ile Ser Glu Ser Ile Glu Val Ser Lys Glu Leu Gln Ile Pro Ala Leu
 660 665 670
 Ser Thr Arg Asp Asn Glu Asn Gln Cys Asp Tyr Arg Thr Gln Asn Val
 675 680 685
 Leu Gly Leu Gln Lys Gln Ile Thr Asn Met Tyr Pro Val Gln Gln Asn
 690 695 700
 Glu Ser Lys Val Asn Lys Lys Leu Arg Gln Lys Val Asn Arg Lys Thr
 705 710 715 720
 Glu Ile Ile Ser Glu Val Asn His Leu Asp Asn Asp Lys Ser Ile Glu
 725 730 735
 Tyr Thr Val Lys Ser His Ser Leu Phe Leu Thr Gln Lys Asp Lys Glu
 740 745 750
 Ile Ile Pro Gly Asn Leu Glu Asp Pro Ser Glu Phe Glu Thr Pro Ala
 755 760 765

Substitute_Sequence_Listing.TXT

Leu Ser Thr Lys Asp Ser Gly Asn Leu Tyr Asp Ser Glu Ile Gln Asn
 770 775 780
 Val Leu Gly Val Lys His Gly His Asp Met Gln Pro Ala Cys Gln Asn
 785 790 795
 Asp Ser Lys Ile Gly Lys Lys Pro Arg Leu Asn Val Cys Gln Lys Ser
 805 810 815
 Glu Ile Ile Pro Glu Thr Asn Gln Ile Tyr Glu Asn Asp Asn Lys Gly
 820 825 830
 Val His Asp Leu Glu Lys Asp Asn Phe Phe Ser Leu Thr Pro Lys Asp
 835 840 845
 Lys Glu Thr Ile Ser Glu Asn Leu Gln Val Thr Asn Glu Phe Gln Thr
 850 855 860
 Val Asp Leu Leu Ile Lys Asp Asn Gly Asn Leu Cys Asp Tyr Asp Thr
 865 870 875 880
 Gln Asn Ile Leu Glu Leu Lys Lys Tyr Val Thr Asp Arg Lys Ser Ala
 885 890 895
 Glu Gln Asn Glu Ser Lys Ile Asn Lys Leu Arg Asn Lys Val Asn Trp
 900 905 910
 Lys Thr Glu Ile Ile Ser Glu Met Asn Gln Ile Tyr Glu Asp Asn Asp
 915 920 925
 Lys Asp Ala His Val Gln Glu Ser Tyr Thr Lys Asp Leu Asp Phe Lys
 930 935 940
 Val Asn Lys Ser Lys Gln Lys Leu Glu Cys Gln Asp Ile Ile Asn Lys
 945 950 955 960
 His Tyr Met Glu Val Asn Ser Asn Glu Lys Glu Ser Cys Asp Gln Ile
 965 970 975
 Leu Asp Ser Tyr Lys Val Val Lys Lys Arg Lys Lys Glu Ser Cys
 980 985 990
 Lys Ala Lys Asn Ile Leu Thr Lys Ala Lys Asn Lys Leu Ala Ser Gln
 995 1000 1005
 Leu Thr Glu Ser Ser Gln Thr Ser Ile Ser Leu Glu Ser Asp Leu

Substitute_Sequence_Listing.TXT

1010
 Lys His Ile Thr Ser Glu Ala Asp Ser Asp Pro Gly Asn Pro Val
 1025 1030 1035
 Glu Leu Cys Lys Thr Gln Lys Gln Ser Thr Thr Thr Leu Asn Lys
 1040 1045 1050
 Lys Asp Leu Pro Phe Val Glu Glu Ile Lys Glu Gly Glu Cys Gln
 1055 1060 1065
 Val Lys Lys Val Asn Lys Met Thr Ser Lys Ser Lys Lys Arg Lys
 1070 1075 1080
 Thr Ser Ile Asp Pro Ser Pro Glu Ser His Glu Val Met Glu Arg
 1085 1090 1095
 Ile Leu Asp Ser Val Gln Gly Lys Ser Thr Val Ser Glu Gln Ala
 1100 1105 1110
 Asp Lys Glu Asn Asn Leu Glu Asn Glu Lys Met Val Lys Asn Lys
 1115 1120 1125
 Pro Asp Phe Tyr Thr Lys Ala Phe Arg Ser Leu Ser Glu Ile His
 1130 1135 1140
 Ser Pro Asn Ile Gln Asp Ser Ser Phe Asp Ser Val Arg Glu Gly
 1145 1150 1155
 Leu Val Pro Leu Ser Val Ser Ser Gly Lys Asn Val Ile Ile Lys
 1160 1165 1170
 Glu Asn Phe Ala Leu Glu Cys Ser Pro Ala Phe Gln Val Ser Asp
 1175 1180 1185
 Asp Glu His Glu Lys Met Asn Lys Met Lys Phe Lys Val Asn Arg
 1190 1195 1200
 Arg Thr Gln Lys Ser Gly Ile Gly Asp Arg Pro Leu Gln Asp Leu
 1205 1210 1215
 Ser Asn Thr Ser Phe Val Ser Asn Asn Thr Ala Glu Ser Glu Asn
 1220 1225 1230
 Lys Ser Glu Asp Leu Ser Ser Glu Arg Thr Ser Arg Arg Arg Arg
 1235 1240 1245

Substitute_Sequence_Listing.TXT

Cys Thr Pro Phe Tyr Phe Lys Glu Pro Ser Leu Arg Asp Lys Met
1250 1255 1260

Arg Arg
1265

<210> 21
<211> 45
<212> PRT
<213> yeast

<400> 21

Met Glu Ser Leu Lys Lys Lys Phe Leu Lys Gln Asn Arg Glu Ile Ile
1 5 10 15

Lys Ile Asn Thr Gln Leu Ser Ile Lys Ile Arg Glu Ser Glu Asn Glu
20 25 30

Ile Gln Asp Leu Ile Gln Glu Asn Phe Thr Leu Lys Ser
35 40 45

<210> 22
<211> 45
<212> PRT
<213> yeast

<400> 22

Val Glu Asp Leu Lys Lys Lys Gln Ile Arg Gln Tyr Lys Glu Ile Ile
1 5 10 15

Arg Ile Ser Lys Ala Gln Ser Ile Arg Ile Lys Glu Leu Gln Leu Glu
20 25 30

Asn Glu Arg Leu Leu Ser Glu Asn Ile Asp Leu Arg Thr
35 40 45

<210> 23
<211> 45
<212> PRT
<213> yeast

<400> 23

Val Glu Asn Ile Arg Gln Ser Tyr Ser Arg Gln Asn Ser Leu Leu Ala
1 5 10 15

Lys Asp Asn Ser Ile Leu Lys Ile Lys Val Asn Ser Leu Glu Lys Lys
20 25 30

Ile Ser Gln Leu Val Gln Glu Asn Val Thr Leu Arg Ser
35 40 45

Substitute_Sequence_Listing.TXT

<210> 24
 <211> 45
 <212> PRT
 <213> Neurospora crassa

<400> 24

Leu Glu Leu Leu Arg Arg Lys Phe Leu Arg Gln Asn Arg Asp Ile Ala
 1 5 10 15

Arg Val Asn Ser Thr Gln Ser Leu Arg Ile Arg Gly Leu Glu Asn Glu
 20 25 30

Cys Ala Arg Leu Leu Ser Glu Asn Leu Glu Leu Arg Gly
 35 40 45

<210> 25
 <211> 45
 <212> PRT
 <213> Dactylicapnos macrocapnos

<400> 25

Gly Ser Lys Val Glu Gln Gln Tyr Lys Leu Leu Asn Ala Glu Leu Met
 1 5 10 15

Asp Gln Val Gln Lys Gln Arg Leu Glu Ile Gly Glu Tyr Arg Lys Arg
 20 25 30

Val Ile Ser Leu Glu Arg Glu Ile Met Asp Ile Arg Glu
 35 40 45

<210> 26
 <211> 27
 <212> PRT
 <213> yeast

<400> 26

Gly Arg Glu Lys Leu Arg Arg Ser Val Lys Val Ile Asn Tyr Ala Ile
 1 5 10 15

Pro Ser Leu Arg Thr Lys Leu Arg Arg Asp Phe
 20 25

<210> 27
 <211> 27
 <212> PRT
 <213> yeast

<400> 27

Pro Asp Gly Arg Ser Arg Arg Glu Arg Lys Lys Val Asn Tyr Ala Leu

Substitute_Sequence_Listing.TXT

1 5 10 15

Pro Gly Leu Arg Thr Lys Leu Arg Arg Asn Phe
20 25

<210> 28
<211> 28
<212> PRT
<213> yeast

<400> 28

Ser Phe Thr Arg Thr Arg Arg Thr Arg Gly Lys Ala Val Asp Tyr Thr
1 5 10 15

Leu Pro Ser Leu Arg Ala Lys Met Arg Arg Pro Ser
20 25

<210> 29
<211> 28
<212> PRT
<213> Neurospora crassa

<400> 29

Glu Thr Ser Arg Pro Ser Arg Arg Ala Arg Ala Ala Ile Ser Tyr Thr
1 5 10 15

Glu Pro Asn Leu Arg Asp Lys Met Arg Arg Pro Thr
20 25

<210> 30
<211> 27
<212> PRT
<213> Dactylicapnos macrocapnos

<400> 30

Asn Ser Ala Arg Pro Ser Arg Ser Cys Arg Pro Thr Ser Leu Val Glu
1 5 10 15

Pro Ser Leu Lys Asn Lys Leu Arg Asn Gly Ser
20 25

<210> 31
<211> 28
<212> PRT
<213> Caenorhabditis elegans

<400> 31

Thr Val Arg Arg Gln Arg Ser Ala Lys Met Asn Ile Lys Ser Leu Lys
1 5 10 15

Substitute_Sequence_Listing.TXT

Glu Pro Ser Gly Lys Asp Lys Leu Arg Arg Pro Gly
20 25

<210> 32
<211> 29
<212> PRT
<213> Arabidopsis thaliana

<400> 32

Thr Val Gly Arg Pro Ser Arg Gln Ala Ala Glu Lys Ile Lys Ser Tyr
1 5 10 15

Lys Glu Pro Ser Leu Lys Glu Lys Met Arg Gly Gly Phe
20 25

<210> 33
<211> 29
<212> PRT
<213> Arabidopsis thaliana

<400> 33

Ser Val Gly Arg Pro Ser Arg His Ala Ala Glu Lys Val Gln Ser Tyr
1 5 10 15

Arg Glu Val Ser Leu Arg Val Lys Met Arg Arg Lys Cys
20 25

<210> 34
<211> 28
<212> PRT
<213> mouse

<400> 34

Ala Val Ala Leu Thr Lys Arg Arg Cys Ser Thr Ile Lys Ser Tyr Lys
1 5 10 15

Glu Pro Thr Leu Ala Ser Lys Leu Arg Arg Gly Asp
20 25

<210> 35
<211> 25
<212> PRT
<213> mouse

<400> 35

His Pro Met Arg Arg Lys Arg Gln Cys Val Pro Leu Asn Leu Thr Glu
1 5 10 15

Pro Ser Leu Arg Ser Lys Met Arg Arg
20 25

Substitute_Sequence_Listing.TXT

<210> 36
 <211> 28
 <212> PRT
 <213> Homo sapiens

<400> 36

Ala Val Ala Leu Pro Lys Arg Arg Cys Thr Ala Ser Val Asn Tyr Lys
 1 5 10 15

Glu Pro Thr Leu Ala Ser Lys Leu Arg Arg Gly Asp
 20 25

<210> 37
 <211> 26
 <212> PRT
 <213> Homo sapiens

<400> 37

Ser Glu Arg Thr Ser Arg Arg Arg Cys Thr Pro Phe Tyr Phe Lys
 1 5 10 15

Glu Pro Ser Leu Arg Asp Lys Met Arg Arg
 20 25

<210> 38
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ?TriplEx

<400> 38
 ctcgggaagc gcgccattgt g 21

<210> 39
 <211> 22
 <212> DNA
 <213> Homo sapiens

<400> 39
 cctggctgaa tcagctttgg tg 22

<210> 40
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 <212> DNA
 <213> Artificial

<220>
 <223> hSgo1

<400> 40
 aagucuacug auaaugucuu att 23

<210> 41

Substitute_Sequence_Listing.TXT

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<211> 23
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<220>
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<400> 41
aagcacuacc acuuugaaua att 23

<210> 42
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<212> DNA
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<220>
<223> hSgo1

<400> 42
gugagccucu gugaauaat t 21

<210> 43
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> hSgo2

<400> 43
gcucucauga acaauaacut t 21

<210> 44
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA,Target1

<400> 44
gagugaucac gauuucuaat t 21

<210> 45
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA,Target2

<400> 45
aacgggcauu ugaaauaгаа a 21

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Substitute_Sequence_Listing.TXT